**BIOTECHNOLOGY
SYSTEMS
BRANCH**

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/517,941_

Source: _PCT/IO_

Date Processed by STIC: _12/28/04_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):**
    U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: *10/517,941*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____ Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

·2_____ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____ Misaligned Amino
Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4_____ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5_____ Variable Length
Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____ PatentIn 2.0
"bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7_____ Skipped Sequences
(OLD RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____ Skipped Sequences
(NEW RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9_____ Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10_____ Invalid <213>
Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11_____ Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12_____ PatentIn 2.0
"bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____ Misuse of n/Xaa
"n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

PCT

RAW SEQUENCE LISTING   DATE: 12/28/2004
PATENT APPLICATION: US/10/517,941   TIME: 11:51:26

Input Set : D:\0077 (OX40).ST25.txt
Output Set: N:\CRF4\12282004\J517941.raw

```
    3  <110> APPLICANT: Crucell Holland B.V.
    4         Bakker, Alexander B.H.
    5         Meester-Rood, Pauline M.L.
    6         Bakker, Adrianus Q.
    8  <120> TITLE OF INVENTION: AGONISTIC BINDING MOLECULES TO THE HUMAN OX40 RECEPTOR
   10  <130> FILE REFERENCE: 0077 WO 00 ORD
C--> 12  <140> CURRENT APPLICATION NUMBER: US/10/517,941
C--> 12  <141> CURRENT FILING DATE: 2004-12-13
   12  <150> PRIOR APPLICATION NUMBER: PCT/NL02/00389
   13  <151> PRIOR FILING DATE: 2002-06-13
   15  <160> NUMBER OF SEQ ID NOS: 54
   17  <170> SOFTWARE: PatentIn version 3.1
   19  <210> SEQ ID NO: 1
   20  <211> LENGTH: 769
   21  <212> TYPE: DNA
   22  <213> ORGANISM: Artificial sequence
   24  <220> FEATURE:
   25  <223> OTHER INFORMATION: scFv SC02008
   27  <220> FEATURE:
   28  <221> NAME/KEY: CDS
   29  <222> LOCATION: (3)..(767)
   30  <223> OTHER INFORMATION:
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   36      1               5                  10                  15
   38  cct gga ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt     95
   39  Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
   40                   20                  25                  30
   42  agc aac tac acg atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg    143
   43  Ser Asn Tyr Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
   44                   35                  40                  45
   46  gag tgg gtc tca gct att agt ggt agt ggt ggt agc aca tac tac gca    191
   47  Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
   48               50                  55                  60
   50  gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac    239
   51  Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
   52           65                  70                  75
   54  acg ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gtg    287
   55  Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
   56  80                  85                  90                  95
   58  tat tac tgt gcc aaa gac cgc tac tcc cag gtg cac tac gcg ttg gat    335
   59  Tyr Tyr Cys Ala Lys Asp Arg Tyr Ser Gln Val His Tyr Ala Leu Asp
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```
60                100               105               110
62 tac tgg ggc cag ggc acc ctg gtg acc gtg ctc gag ggt acc gga ggt    383
63 Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly
64                115               120               125
66 tcc ggc gga acc ggg tct ggg act ggt acg agc gag ctc gac atc cag    431
67 Ser Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln
68           130               135               140
70 atg acg cag tct cca gac tca ctg ccc gtc acc cct gga gag ccg gcc    479
71 Met Thr Gln Ser Pro Asp Ser Leu Pro Val Thr Pro Gly Glu Pro Ala
72      145                150               155
74 tcc atc tcc tgc agg tct agt cag agc ctc ctg cat agt aat gga tac    527
75 Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr
76 160               165               170               175
78 aac tat ttg gat tgg tac ctg cag aag gca ggg cag tct cca cag ctc    575
79 Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Ala Gly Gln Ser Pro Gln Leu
80                180               185               190
82 ctg atc tat ttg ggt tct aat cgg gcc tcc ggg gtc cct gac agg ttc    623
83 Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe
84           195               200               205
86 agt ggc agt gga tca ggc aca gat ttt aca ctg aaa atc agc aga gtg    671
87 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
88           210               215               220
90 gag gct gag gat gtt ggg gtt tat tac tgc cag cag tac tac aac cac    719
91 Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr Tyr Asn His
92      225                230               235
94 ccg acg acc ttc ggc cag ggc acc aaa ctg gaa atc aaa cgc gcg gcc    767
95 Pro Thr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
96 240                245               250               255
98 gc                                                                 769
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102 <211> LENGTH: 255
103 <212> TYPE: PRT
104 <213> ORGANISM: Artificial sequence
106 <220> FEATURE:
107 <223> OTHER INFORMATION: scFv SC02008
109 <400> SEQUENCE: 2
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112 1               5                   10                  15
115 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
116           20                  25                  30
119 Asn Tyr Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
120      35                  40            45
123 Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp
124   50                  55                  60
127 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
128 65                  70                  75                  80
131 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
132                85                  90                  95
135 Tyr Cys Ala Lys Asp Arg Tyr Ser Gln Val His Tyr Ala Leu Asp Tyr
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what is the source? (handwritten annotation)

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136                 100                 105                 110
139 Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser
140         115                 120                 125
143 Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln Met
144     130                 135                 140
147 Thr Gln Ser Pro Asp Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser
148 145                 150                 155                 160
151 Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn
152             165                 170                 175
155 Tyr Leu Asp Trp Tyr Leu Gln Lys Ala Gly Gln Ser Pro Gln Leu Leu
156         180                 185                 190
159 Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser
160         195                 200                 205
163 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu
164     210                 215                 220
167 Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr Tyr Asn His Pro
168 225                 230                 235                 240
171 Thr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
172             245                 250                 255
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176 <211> LENGTH: 775
177 <212> TYPE: DNA
178 <213> ORGANISM: Artificial sequence
180 <220> FEATURE:
181 <223> OTHER INFORMATION: scFv SC02009
183 <220> FEATURE:
184 <221> NAME/KEY: CDS
185 <222> LOCATION: (3)..(773)
186 <223> OTHER INFORMATION:
189 <400> 3
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192    1               5               10              15
194 cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc        95
195 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
196             20              25              30
198 agc ggc tac tct atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg       143
199 Ser Gly Tyr Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
200         35              40              45
202 gag tgg gtt ggc cgt act aga aac aaa gct aac agt tac acc aca gaa       191
203 Glu Trp Val Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu
204     50              55              60
206 tac gcc gcg tct gtg aaa ggc aga ttc acc atc tca aga gat gat tca       239
207 Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
208     65              70              75
210 aag aac tca ctg tat ctg caa atg aac agt ctg aga gcc gag gac aca       287
211 Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
212 80              85              90              95
214 gcc gtg tat tac tgt gcc aaa gac cgc tac gtc aac acg tcg aac gcg       335
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RAW SEQUENCE LISTING   DATE: 12/28/2004
PATENT APPLICATION: US/10/517,941   TIME: 11:51:26

Input Set : D:\0077 (OX40).ST25.txt
Output Set: N:\CRF4\12282004\J517941.raw

215 Ala Val Tyr Tyr Cys Ala Lys Asp Arg Tyr Val Asn Thr Ser Asn Ala
216   100   105   110
218 ttc gat tac tgg ggc cag ggc acc ctg gtg acc gtg ctc gag ggt acc   383
219 Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr
220   115   120   125
222 gga ggt tcc ggc gga acc ggg tct ggg act ggt acg agc gag ctc gac   431
223 Gly Gly Ser Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp
224   130   135   140
226 atc cag atg aca cag tct cca gac tca ctg ccc gtc acc cct gga gag   479
227 Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Pro Val Thr Pro Gly Glu
228   145   150   155
230 ccg gcc tcc atc tcc tgc aga tct agt cag agc ctc ctg cat agt aat   527
231 Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn
232 160   165   170   175
234 gga tac aac tat ttg gat tgg tac ctg cag aag cca ggg cag tct cca   575
235 Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro
236   180   185   190
238 cag ctc ctg atc tat ttg ggt tct aat cgg gcc tcc ggg gtc cct gac   623
239 Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp
240   195   200   205
242 agg ttc agt ggc agt gga tca ggc aca gat ttt aca ctg aaa atc agc   671
243 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser
244   210   215   220
246 aga gtg gag gct cac cat gtt ggg gtt tat tac tgc cag cag tac ccg   719
247 Arg Val Glu Ala His His Val Gly Val Tyr Tyr Cys Gln Gln Tyr Pro
248   225   230   235
250 ctg ggc ccg ccc acc ttc ggc cag ggc acc aaa ctg gaa atc aaa cgc   767
251 Leu Gly Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
252 240   245   250   255
254 gcg gcc gc   775
255 Ala Ala
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260 <211> LENGTH: 257
261 <212> TYPE: PRT
262 <213> ORGANISM: Artificial sequence
264 <220> FEATURE:
265 <223> OTHER INFORMATION: scFv SC02009
267 <400> SEQUENCE: 4
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270 1   5   10   15
273 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
274   20   25   30
277 Gly Tyr Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
278   35   40   45
281 Trp Val Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu Tyr
282   50   55   60
285 Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
286 65   70   75   80
289 Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala

```
290                 85              90              95
293 Val Tyr Tyr Cys Ala Lys Asp Arg Tyr Val Asn Thr Ser Asn Ala Phe
294             100             105             110
297 Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly
298         115             120             125
301 Gly Ser Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile
302     130             135             140
305 Gln Met Thr Gln Ser Pro Asp Ser Leu Pro Val Thr Pro Gly Glu Pro
306 145             150             155             160
309 Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly
310             165             170             175
313 Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln
314             180             185             190
317 Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg
318         195             200             205
321 Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg
322     210             215             220
325 Val Glu Ala His His Val Gly Val Tyr Tyr Cys Gln Gln Tyr Pro Leu
326 225             230             235             240
329 Gly Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala
330             245             250             255
333 Ala
337 <210> SEQ ID NO: 5
338 <211> LENGTH: 736
339 <212> TYPE: DNA
340 <213> ORGANISM: Artificial sequence
342 <220> FEATURE:
343 <223> OTHER INFORMATION: scFv SC02010
345 <220> FEATURE:
346 <221> NAME/KEY: CDS
347 <222> LOCATION: (3)..(734)
348 <223> OTHER INFORMATION:
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354    1               5              10              15
356 cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc     95
357 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
358             20              25              30
360 agc ggc tac cct atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg    143
361 Ser Gly Tyr Pro Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
362             35              40              45
364 gag tgg gtg gca gtt ata tca tat gat gga agt aat aaa tac tac gca    191
365 Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
366         50              55              60
368 gac tcc gtg aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac    239
369 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
370     65              70              75
372 acg ctg tat ctg caa atg aac agc ctg aga gct gag gac aca gcc gtg    287
```

Important

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY   DATE: 12/28/2004
PATENT APPLICATION: **US/10/517,941**   TIME: 11:51:27

Input Set : **D:\0077 (OX40).ST25.txt**
Output Set: **N:\CRF4\12282004\J517941.raw**

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:33 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:30
L:189 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:186
L:351 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:348
L:505 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:502
L:659 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:656
L:813 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:810
L:969 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:966
L:1123 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:1120
L:2157 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:33,Line#:2154
L:2199 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:35,Line#:2196
L:2241 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:37,Line#:2238
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